

**IN THE SPECIFICATION:**

Please replace the paragraph beginning on page 19 line 9 with the following:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) ([\[\[www.\]\]available on the worldwide web at ddbj.nig.ac.jp](http://www.ddbj.nig.ac.jp)); Genebank ([\[\[www.\]\] available on the worldwide web at the ncbi website at: /Web/Search/Index.html](http://www.ncbi.nlm.nih.gov/Web/Search/Index.html)); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) ([\[\[www.\]\] available on the worldwide web at ebi.ac.uk/ebi\\_docs/embl\\_db/embl-db.html](http://www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html)). Other appropriate databases include dbEST ([\[\[www.\]\] available on the worldwide web at the ncbi website at:/dbEST /index.html](http://www.ncbi.nlm.nih.gov/dbEST/index.html)), SwisProt ([\[\[www.\]\] available on the worldwide web at ebi.ac.uk/ebi\\_docs/swisprot\\_db/swisshome.html](http://www.ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html)), PIR ([\[\[www.\]\] available on the worldwide web at nbrt.georgetown.edu/pir](http://www.nbrt.georgetown.edu/pir)), and The Institute for Genome Research ([\[\[www.\]\] available on the worldwide web at tigr.org/tdb/tdb.html](http://www.tigr.org/tdb/tdb.html)).

Please replace the paragraph beginning on page 21, line 8, and continuing through page 22, line 2, with the following:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage

the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available by anonymous ftp at: ~~ftp.ebi.ac.uk~~ ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms and is available by anonymous ftp at the ncbi website at: ~~ncbi.nlm.nih.gov~~ nlm.nih.gov (directory/pub/macaw).

Please replace the paragraph beginning on page 74, line 17 with the following:

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure to with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (~~www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi~~ available on the worldwide web at genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (~~www-genome.wi.mit.edu/cgi-bin/www-STS\_Pipeline~~ available on the worldwide web at genome.wi.mit.edu/cgi-bin/www-STS\_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.